

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 3, 2003, 12:50:42 ; Search time 2379 Seconds

(without alignments)
17563.832 Million cell updates/sec

Title: US-10-047-593-5

Sequence: 1 gcggcgccgctaacagcattc.....cgctctaggaagggtcacgt 2580

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_esbca:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	511	19.8	547	17	BH619556 1007059P1
C 2	427.4	16.6	717	17	BH838358 LMCR10001
C 3	338	13.1	677	17	BH800632 1008125G0
C 4	335.4	13.0	727	17	BH838131 LMCR10000
C 5	323.6	12.5	485	17	BH779556 f2mb014f0
C 6	319.4	12.4	509	17	BH127535 G-1h2.r M

Result No.	Score	Query Match	Length DB	ID	Description
C 7	309.8	12.0	744	17	BH837342
C 8	308.6	12.0	617	17	BH774273
C 9	305.2	11.8	847	17	BH129403
C 10	297	11.5	710	17	BH837822
C 11	289.2	11.2	709	17	BH837873
C 12	288.4	11.2	549	17	BH774554
C 13	284.2	11.0	620	17	BH836722
C 14	283.2	11.0	813	17	BH839302
C 15	282.2	10.9	618	17	BH873660
C 16	281.6	10.9	606	17	BH873437
C 17	278	10.8	378	17	BH772161
C 18	277.2	10.7	546	17	BH785550
C 19	277.2	10.7	719	17	BH838303
C 20	273.2	10.6	522	17	BH130068
C 21	269.8	10.5	533	17	A2920086
C 22	268.4	10.4	729	17	BH839096
C 23	266.6	10.3	535	17	BH222651
C 24	266.2	10.3	926	17	BH128342
C 25	263.2	10.2	844	17	BH129231
C 26	262.2	10.2	697	17	BH837902
C 27	260.4	10.1	995	17	BH129116
C 28	252.6	9.8	592	17	BH786386
C 29	251.6	9.8	455	17	BH837520
C 30	247.8	9.6	605	17	BH782172
C 31	246.6	9.6	445	17	A2921056
C 32	243.4	9.5	280	17	BH619555
C 33	243.4	9.4	593	17	BH773010
C 34	243.4	9.4	831	17	BH127782
C 35	242.6	9.4	455	17	BH807089
C 36	240.8	9.3	867	17	BH127930
C 37	240	9.3	742	17	BH140491
C 38	239	9.3	473	17	BH779949
C 39	236.4	9.2	325	17	BH128264
C 40	233	9.0	729	17	BH876361
C 41	232.2	9.0	925	17	BH128803
C 42	229.2	8.9	681	17	BH255865
C 43	228.8	8.9	557	17	BH773008
C 44	225.8	8.8	443	17	BH129668
C 45	224.4	8.7	735	17	BH836993

ALIGNMENTS

RESULT 1
BH619556/c
LOCUS 1007059P1.y1 1007 - Rescuedu Grid H Zea mays genomic, DNA
DEFINITION
ACCESSION BH619556
VERSION BH619556.1 GI:18430399
KEYWORDS
SOURCE
ORGANISM
Zea mays.
Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 547)
Walbot, V.
Maize genomic sequences found using engineered Rescuedu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1007059 column: 19
Class: transposon-tagged
Location/Qualifiers

FEATURES

source
1. .547
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1007" - RescuedMu Grid H"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: RescuedMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescuedMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuedMu, go to the site 'www.zmhd.iastate.edu' and follow the links for 'RescuedMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 179 a 114 c 97 g 157 t
ORIGIN

Query Match 19 8%; Score 511; DB 17; Length 547;
Best Local Similarity 97.1%; Pred. No. 2.1e-113;
Matches 531; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 1521 CAATTTCATTTTATATTTTCTTCCATTAAC-AAACCTAAGTACTGTTT 1579
DB 547 CATTTCATTTTATATTTTCTTCCATTAACAAACCTAAGTACTGTTT 488
QY 1560 TGGACCTTTGACACATACCTTTTAAAGTATTTACAAATTTAGCTGTATGTAAC 1639
DB 487 TGGACCTTTGACACATACCTTTTAAAGTATTTACAAATTTAGCTGTATGTAAC 428
QY 1640 AAACCTAATTTGAGAGAGGCTGATTTGAGAGAAAGTCTGGCTGATTTCAATTGGAC 1699
DB 427 AAGCTAATTTGAGAGAGGCTGATTTGAGAGAAAGTCTGGCTGATTTCAATTGGAC 368
QY 1700 GAAATCGATTTTAAATCTGCTGTTGATTAATTTCTAGCTTACACGCTTGAACCG 1759
DB 367 GAAATCGATTTTAAATCTGCTGTTGATTAATTTCTAGCTTACACGCTTGAACCG 308
QY 1760 CCTAGAGCTGTGGAATTTCCCTTATGATTTATAGAGTGTGTTTGTACAGTT 1819
DB 307 CCTAGAGCTGTGGAATTTCCCTTATGATTTATAGAGTGTGTTTGTGACGTT 248
QY 1820 TATTTACGATTCATTTACGATTTTATTTAGGATTCGTTGACATTAATCTTCACTTTC 1879
DB 247 TATTTACGATTCATTTACGATTTTATTTAGGATTCGTTGACATTAATCTTCACTTTC 188
QY 1880 TTTTAAATAGTACAAAGAACTTTTACACACCTTCTGAGGATTAACGAAACATGAGAC 1939
DB 187 TTTTAAATAGTACAAAGAACTTTTACACACCTTCTGAGGATTAACGAAACATGAGAC 128
QY 1940 AATATGATTTTGAAGAAATATTTGACAGATTAAGTGTGTGGGACCTGTAGAGACTAG 1999
DB 127 AATATGATTTTGAAGAAATATTTGACAGATTAAGTGTGTGGGACCTGTAGAGACTAG 68
QY 2000 AGAGATGAGAGACGACGCGAGCAAGACCTTCCGATTTCCGTGACGCTCCTGG 2059
DB 67 AGAGATGAGAGACGACGCGAGCAAGACCTTCCGATTTCCGTGACGCTCCTGG 8
QY 2060 TCAGGGC 2066
DB 7 TCAGGGC 1

RESULT 2
BH838358 717 bp DNA linear GSS 28-MAY-2002
LOCUS LMCR100011F01f Zea mays L. Zea mays genomic clone LMCR100011F01f,
DEFINITION
DNA sequence.

ACCESSION BH838358
VERSION BH838358.1 GI:21236236
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 717)
AUTHORS Kim, S.W., Yu, Y., Lee, M.C., Main, D. and Wing, R.A.
TITLE Methy1-Filteration genomic sequence from maize
JOURNAL Unpublished (2002)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Total High Quality bases = 428
Seq primer: TAATACACTCACTATAGG
Class: shotgun
High quality sequence start: 44
High quality sequence stop: 686.
Location/Qualifiers

FEATURES

source

1. .717
/organism="Zea mays"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="LMCR100011F01f"
/clone_lib="Zea mays L."
/tissue_type="leaf"
/lab_host="DH10B"
/note="Vector: pGEM-T easy; Site 1: Mcr BC; Methy1-filteration library; Nuclei DNA was completely digested with Mcr BC, size fractionated and transformed to E.Coli.DH10B."

BASE COUNT 147 a 223 c 169 g 175 t 3 others
ORIGIN

Query Match 16.6%; Score 427.4; DB 17; Length 717;
Best Local Similarity 90.5%; Pred. No. 4.4e-93;
Matches 497; Conservative 0; Mismatches 31; Indels 21; Gaps 3;

QY 37 TTGGATCTCTTCTTATTTTGGGAAAGCCGACCTTTGGGACCGTTGGCGCA 96
DB 149 TGGGATCTCTTCTTATTTTGGGAAAGCCGACCTTTGGGACCGTTGGCGCA 208
QY 97 CCGACACCTGTCGGGTGACACCGGACAGTCAGTGGCCCTTCCGACGTTGGCTCGGC 156
DB 209 CCGACACCTGTCGGGTGACACCGGACAGTCAGTGGCCCTTCCGACGTTGGCTCGGC 268
QY 157 CACGCTTTCGCGGAGATTCGCGCGGACAGCGTTGGCCCGACCGACGTTGGCTCACGG 216
DB 269 CACGCTTTCGCGGAGATTCGCGCGGACAGCGTTGGCCCGACCGACGTTGGCTCACGG 327
QY 217 ACAGTCCGTGCAACCAAGACAGTCGCGGTATTAATGACGTCGCGGTAAATCACTTC 276
DB 328 -----GACAGTCGCGGTATTAATGACGTCGCGGTAAATCACTTC 369
QY 277 CGAGAGCAAGATTTGCTGAGCGACCTGCGGACCGGACACCTGTCGCGGTAAACACC 336
DB 370 CGAGAGCAAGATTTGCTGAGCGACCTGCGGACCGGACACCTGTCGCGGTAAACACC 429
QY 337 GGCAGATCCGCTGACCCAGTCAAGCTGACTTTGGCTGAACAAAGTCATCTTAATGTC 396
DB 430 GGCAGATCCGCTGACCCAGTCAAGCTGACTTTGGCTGAACAAAGTCATCTTAATGTC 489
QY 397 AACTGATTTTCTGTTTCCAGACATTAAGCAATTAATGTCCTTAACAAATGTA 456
DB 490 AACTGATTTTCTGTTTCCAGACATTAAGCAATTAATGTCCTTAACAAATGTA 548
QY 457 TTAATTTGAGAAACATACCTTTAATCTTGTGTTGTAATTTGTCACCAATTAACACTTG 516

Db 549 CTAACTTGAGAAACATCTTTACTTGAATTTGTCTTGTCCACCATTTTACACTTA 608
 Qy 517 GGAC-1TTGTTGGACACTAAATCACCATAACTTTGAATAGCCCAAGGACATT 575
 Db 609 GGCACTTTGTGTGGACACTAAATCACCATAACTTTGAATAGCCCAAGGACATT 668
 Qy 576 CCGCTTTCA 584
 Db 669 TCCCTTCA 677

RESULT 3
 BH800632/c 677 bp DNA linear GSS 25-APR-2002
 LOCUS 1008125G09.x1 1008 - Rescuemu Grid I Zea mays genomic, DNA
 DEFINITION
 sequence.
 ACCESSION BH800632
 VERSION BH800632.1 GI:20312874
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 677)
 Walbot, V.
 Maize genomic sequences found using engineered Rescuemu transposon
 Unpublished (2001)
 CONTACT: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 723 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 plate: 1008125 row: 15
 Class: transposon-tagged.
 Location/Qualifiers
 1..677
 /organism="Zea mays"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /clone_lib="1008 - Rescuemu Grid I"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: leaf; Vector: Rescuemu (engineered from
 pBluescript backbone); Site_1: BamHI; Site_2: BglII;
 Rescuemu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on Rescuemu, go to the web
 site www.zmhd.jaxstate.edu and follow the links for
 'Rescuemu.' Grid I was grown at Berkeley in 2001. DNA was
 extracted from leaf punches, double digested using BamHI
 and BglII, and ligated to form circular plasmids. DH10B
 cells were transformed and then screened on LB plates with
 ampicillin."

BASE COUNT 201 a 134 c 160 g 182 t
 ORIGIN
 Query Match 13.1%; Score 338; DB 17; Length 677;
 Best Local Similarity 97.0%; Pred. No. 2,4e-71;
 Matches 355; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1922 TAACAGAAAACTGACATATGATTTGAAAAAAGAAATGACAGATAAGCTGT 1981
 Db 366 TAACAGAAAACTGACATATGATTTGAAAAAAGAAATGACAGATAAGCTGT 307
 Qy 1982 GGGAGCCGTAGAGACTAGAGAGATGAGACGCGCAGAGAGAGCTTGCAGATTG 2041

Db 306 GGGAGATGGGACCCGTAGAGAGATGAGACGAGCCGAGAGAGCTTGCAGATTG 247
 Qy 2042 CCGTCAGAGCTACCTGTCAGAGGCTGACTTGAAGAGATAGCAGAGGAGGCTCAG 2101
 Db 246 CCGTCAGAGCTACCCGTGTCAGAGGCTGACTTGAAGAGATAGCAGAGGAGGCTCAG 187
 Qy 2102 GTTTCCCTCAATAGCGCGGAAATATCTGAGATTTCTTGA-TTTTTTTACTTGTAT 2160
 Db 186 GTTTCCCTCAATAGCGCGGAAATATCTGAGATTTCTTGA-TTTTTTTACTTGTAT 127
 Qy 2161 TCTATTCCTCTCCGCGGCTCTAGTCTATTCTCTCTCCGTCGAGTGTGCTTC 2220
 Db 126 TCTATTCCTCTCCGCGGCTCTAGTCTATTCTCTCTCCGTCGAGTGTGCTTC 67
 Qy 2221 TTGATTCACCTTTTCCCGCATCTCTATCTCCCTTCCAGCAGCACTGGCTTCC 2280
 Db 66 TTGATTCACCTTTTCCCGCATCTCTATCTCCCTTCCAGCAGCACTGGCTTCC 7
 Qy 2281 GGACTC 2286
 Db 6 GGACTC 1

RESULT 4
 BH838131 727 bp DNA linear GSS 28-MAY-2002
 LOCUS LMCRI00008H10f Zea mays L. Zea mays genomic clone LMCRI00008H10f,
 DEFINITION
 DNA sequence.
 ACCESSION BH838131
 VERSION BH838131.1 GI:21236009
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 727)
 Kim, S.W.; Yu, Y.; Lee, M.C.; Main, D. and Wang, R.A.
 Methyl-filtration genomic sequence from maize
 Unpublished (2002)
 CONTACT: Wang RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rtwing@clemson.edu
 Total High Quality bases = 561
 Seq primer: TAATACGACTCACTATAGG
 Class: shotgun
 High quality sequence start: 30
 High quality sequence stop: 714.
 Location/Qualifiers
 1..727
 /organism="Zea mays"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_lib="LMCRI00008H10f"
 /clone_lib="Zea mays L."
 /tissue_type="leaf"
 /lab_host="DH10B"
 /note="Vector: pGEM-T easy; Site 1: Mcr BC;
 Methyl-filtration library. Nuclei DNA was completely
 digested with Mcr BC, size fractionated and transformed
 to E. Coli DH10B."

FEATURES
 source
 BASE COUNT 161 a 211 c 173 g 177 t 5 others
 ORIGIN
 Query Match 13.0%; Score 335.4; DB 17; Length 727;
 Best Local Similarity 81.5%; Pred. No. 1e-70;
 Matches 446; Conservative 0; Mismatches 76; Indels 25; Gaps 4;

QY 39 CGAGTCTCTTCTTATTGCGAGCCGACCGTGGC-GCTTTGAGCCGTTGGCGAC 97
 125 CTGATTTCTTCTTAAATGCGAAGCCGACCGTTGGCAGACTGGACCGTTGGCGAC 184
 QY 98 CGGACATCTCCGCTGACACCGGACGAGTGGCCCTCCGACCGTTGGCGAC 157
 185 CGGACA-TGTCGGTGGACACCGGACGAGTGGTGGACATCTTTAGCCGTTGGCGAC 243
 QY 158 ACGTGTTCGCGCGATCGCGGACGAGCCGTTGGCCGACCGTGGCTTCACCGA 217
 244 ATGATCTTGGCGAGATTTGGCGCGCCGCTGGCCGCGACCGTTGGCTTCACCGA 303
 QY 218 CAGTCCGCTGACACCGACAGTCCGTTGAATTATAGCCGTTGGCTTCACCTCC 277
 304 CAGTCCGCTGACACCGACAGTCCGTTGAATTATAGCCGTTGGCTTCACCTCC 363
 QY 278 GAGAGCGAGCATTTGCGCTGACCGCTGGCGACCGACACTGTCCGTTGAACCA 337
 364 GAGAGCGCGCATTTGCGCTGACCGCTGGCGACCGACACTGTCCGTTGAACCA 423
 QY 338 GACAGTCCGCTGACCGCAGTCAAGCTGATTTGGCTGAACCAAGTCACTTTAGTCCA 397
 424 CTCAGCAGATTTCTTGGCTGCTGACGACCA-----GACATTTTCCA 462
 QY 398 ACTGATTTTCTTCTTCTTCCGACCTTGAACCAATATAGTCTCTTAAACAAATGAT 457
 463 ATTGAATTTTCTTCTTCTTCCGACCTTGAACCAATATAGTCTCTTAAACAAATGAT 522
 QY 458 TAATCTGAGAAACATCTTAACTTGTGTTGACTTTGACCACTTTTACACTTTG 517
 523 TTAGCTGAGAAACATCTTAACTTGTGTTGACTTTGACCACTTTTACACTTTG 582
 QY 518 GCATCTGTTGAGACATTAATCAACAAATCTTGAATGCGCCAGGCGACATTTCC 577
 583 ACATCTGTTGAG--ACTTAAATCAACAAACATTAAGAAATGCGCCAGGCGACATTTCC 640
 QY 578 CTTTCAA 584
 641 CTTTCAA 647

RESULT 5
 BH779556/c 485 bp DNA linear GSS 28-MAR-2002
 LOCUS f2mb014f016e12f0 f2mb filtered library Zea mays genomic clone
 DEFINITION f2mb014f016e12 5', DNA sequence.

ACCESSION BH779556
 VERSION BH779556
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.

REFERENCE 1 (bases 1 to 485)
 AUTHORS Budiman, M.A., Freese, R.G., Bedell, J.A., Nunberg, A.N. and Lakey, N.D.
 TITLE Genethresher methylation filtered genomic sequences from maize
 JOURNAL Unpublished (2002)
 COMMENT Contact: Bedell JA
 Orion Genomics, LLC
 4041 Forest Park Ave, St. Louis, MO 63108, USA
 Tel: 314 615 6979
 Fax: 314 615 5975
 Email: jbedell@oriongenomics.com
 Plate: f2mb014f016 row: e column: 12
 Seq primer: M13 forward
 Class: shotgun

High quality sequence stop: 485.

FEATURES
 source 1.485
 Location/Qualifiers
 /organism="Zea mays"
 /cultivar="MO17"
 /db_xref="taxon:4577"

/clone="f2mb014f016e12"
 /clone.lib="f2mb filtered library"
 /note="Organ: leaf; Vector: pBCK(-); Site 1: HincII; DNA
 prepared from purified nuclei was randomly sheared,
 end-repated, size fractionated to enrich for the 0.5 to
 5 kb fraction, ligated into HincII-digested pBCK(-)
 vector and electroporated into E. coli cells."
 BASE COUNT 125 a 97 c 145 g 117 t 1 others
 ORIGIN
 Query Match 12.5%; Score 323.6; DB 17; Length 485;
 Best Local Similarity 84.5%; Pred. No. 7.5e-68;
 Matches 393; Conservative 0; Mismatches 55; Indels 17; Gaps 2;

QY 126 TCAGTGGCCCCCTTCCGACCGTTGGCTGGCGACGTTGTTGGCCGAGTCCGCGGACGA 185
 485 TCCGGGCCCCCTTCCGACCGTTGGCTGGCGACGTTGTTGGCCGAGTCCGCGGACG 430
 QY 186 CCGTTGGCCCCCGACCGACCGTTGGCTCACCGACGTTCCGTTGACACCGACAGTCCGAT 245
 429 -----CCGACCGTTGGCTCACCGACGTTCCGTTGACACCGACAGTCCGAT 382
 QY 246 GAATTATAGCCGTAGCCGTTATCACTTCCGAGAGAGAGAGTGGCTGAGCCAGCC 305
 381 GAATTATAGCTGTAGCGCCGTTAATTTGTTCCGATAGCGCAAGTTGGCTGATTTAGCC 322
 QY 306 TGGCGACCGGACGACGTTCCGTTGAACCAACGAGTCCGTTGACCGACGAGTCAAGCTG 365
 321 TGGCACACGACGACGTTCCGTTGAACCAACGAGTCCGTTGACCGACGAGTCAAGCTG 262
 QY 366 ACTTGGCTGAACCAAGTCACTTTAGTTCAACTTTGTTCTGTTTCCAGACACTTA 425
 261 GCTTGGCTGAACCAAGGCT-TATCTCTCTCAATTTGTTTCTGTTTCCAGACACTTA 203
 QY 426 GACACAAATCAATAGCTCTTAAACAAATGATTAATTCGAGAAACATACCTTTACTT 485
 202 GACACAAATCAATAGCTCTTAAACAAATGATTAATTCGAGAAACATACCTTTACTT 143
 QY 486 GATTGTACTTTGTTCCACCACTTTAACTTGGGCACTTGTGTTGACACTTAATCAACCA 545
 142 GATTGTACTTTGTTCCACCACTTTAACTTGGGCACTTGTGTTGACACTTAATCAACCA 83
 QY 546 AATCTTGAATAGCGCCAGGCGACATTTCCCTTCAACAGTCC 590
 82 AACACTTGAATAGCGCCAGGCGACATTTCCCTTCAACAGTCC 38

RESULT 6
 BH127535 509 bp DNA linear GSS 23-JUL-2001
 LOCUS G-1h2.r Maize Random Small-insert Genomic Library Zea mays genomic
 DEFINITION clone G-1h2 both, DNA sequence.
 ACCESSION BH127535
 VERSION BH127535
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.

REFERENCE 1 (bases 1 to 509)
 AUTHORS Meyers, B.C., Tingey, S.V. and Morgante, M.
 TITLE Abundance, distribution and transcriptional activity of repetitive
 elements in the maize genome
 JOURNAL Genome Res. 11 (10), 1660-1676 (2001)
 MEDLINE 21475670
 COMMENT Contact: Morgante M
 Suite 200
 Dupont Genomics
 PO Box 6104, Newark, DE 19714-6104, USA
 Tel: 302 631 2638
 Fax: 302 631 2607
 Email: Michele.morgante@usa.dupont.com

Sequences were trimmed to include only high quality bases; forward and reverse reads were assembled when significant overlaps were detected.

```
seq primer: M13reverse
Class: shotgun.
```

Locat

FEATURES	Location/Qualifiers
source	1. .509

```

BASE COUNT
ORIGIN
101 a 156 c 126 g 126 t

```

AUTHORS R.M.S.W., Yu,Y., Lee,M.C., Main,D. and Wing,R.A
TITLE Methyl-filtration genomic sequence from maize
JOURNAL Unpublished (2002)
COMMENT Contact: Wing RA

FEATURES	Location/Qualifiers
source	1. .744

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/organism="Zea mays"
/strain="B73"
/db_xref="taxon:4577"
/clone="LMCR50012G12F"
/clone_lib="Zea mays L."
/clone_type="Leaf"
/lab_host="DH10B"
/notes="Vector: pGEM-T easy; Site 1: Mcr BC;
MethyI-filtration library, Nuclei DNA was completely
digested with Mcr BC, size fractionated and transformed
to E.Coli.DH10B."

```

ACCESSION BH774273 GI:19776302
 VERSION BH774273.1
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
 AUTHORS Budiman, M.A., Freese, R.G., Bedell, J.A., Nunberg, A.N. and Lakey, N.D.
 TITLE Genethresher methylation filtered genomic sequences from maize
 JOURNAL Unpublished (2002)
 COMMENT Contact: Bedell JA
 Orlon Genomics, LLC
 4041 Forest Park Ave, St. Louis, MO 63108, USA
 Tel: 314 615 6979
 Fax: 314 615 5975
 Email: jbedell@orlongenomics.com
 Plate: um003f006 row: b column: 02
 Seq primer: SK reverse
 Class: Shotgun
 High quality sequence stop: 617.
 Location/Qualifiers
 1. 617
 /organism="Zea mays"
 /cultivar="M017"
 /db_xref="taxon:4577"
 /clone="um003f006b02"
 /note="Organ: leaf; Vector: pBCKS(-); Site: 1: HincII; DNA end repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCKS(-) vector and electroporated into E. coli cells."

BASE COUNT 155 a 155 c 181 g 126 t

ORIGIN

Query Match 12.0%; Score 308.6; DB 17; Length 617;
 Best Local Similarity 77.5%; Pred. No. 3.3e-64;
 Matches 441; Conservative 0; Mismatches 114; Indels 14; Gaps 5;

39 CGGATCTCTCTCTTATTGCGAAGCCGACCGTGGCGCT-TTGGAGCGGTGGCGCAC 97
 607 CGGATCTCTCTCTTAAATGGGAAGCCGATCTGGAGACCGTGGCGCAC 548
 98 CGGACACTGTCGGTGGCACACCGGACAGTCAAGTCCCTTCCGACCGTGGCGTCCGCC 157
 547 CGGACA-TGTTGCGTGACACCGGACAGTCCGCTCCCTTCGACCGTGGCGTCCGCC 489
 158 AGTGTTCGCGCGGATCGCGGACAGCCGTTGGCCCGACCGGACCGTGGCGTCCGCC 217
 488 AGGTGTCGCGCGGACAGTCCGCGGACAGTCCGCTCCGCGGACCGTGGCGTCCGCC 429
 218 CAGTCGCGTGACACCGGACAGTCCGCGGATTAATTAAGCGGTAAGCGGTAATTAATTA 277
 428 CAGTCGCGTGACACCGGACAGTCCGCGGATTAATTAAGCGGTAAGCGGTAATTAATTA 369
 278 GAGAGGAGCAAGTTCGCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGAC 337
 368 GAGAGGAGCGCTTCGCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGAC 309
 338 GACAGTCGCGTGACACCGGACAGTTCGCGGATTAATTAAGCGGTAATTAATTAATTA 397
 308 GACAGTCGCGTGACACCGGACAGTTCGCGGATTAATTAAGCGGTAATTAATTAATTA 249
 398 ACTTGAATTTCTCTCTTTCAGACTTGAACAATTAATTAATTAATTAATTAATTAAT 457
 248 TTTCTTTCTCTCTCTTTCAGACTTGAACAATTAATTAATTAATTAATTAATTAAT 189
 458 TAATTTTGAGAA-CATACCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 506
 188 TAAGACTTGAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 129

507 TTAACACTTGGGACCTGTGTGGACCTAATACCAAAATTAATTAATTAATTAATTAAT 566
 128 TTACACTTGAACACCTGTGTGG-CATCAATACCAAAATTAATTAATTAATTAATTAAT 70

567 GGCACATTTTCCCTTTCAACACTCGGATG 595
 69 GGCACATTTTCCCTTTCAACACTCGGATG 41

RESULT 9
 BH129403 847 bp DNA linear GSS 23-JUL-2001
 LOCUS G-5c8 Maize Random Small-insert Genomic Library Zea mays genomic
 DEFINITION clone G-5c8 both, DNA sequence.
 ACCESSION BH129403
 VERSION BH129403.1 GI:14997719
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
 AUTHORS Meyers, B.C., Tingey, S.V. and Morgante, M.
 TITLE Abundance, distribution and transcriptional activity of repetitive elements in the maize genome
 JOURNAL Genome Res. 11 (10), 1660-1676 (2001)
 MEDLINE 21475670
 COMMENT Contact: Morgante M
 Suite 200
 Dupont Genomics
 PO Box 6104, Newark, DE 19714-6104, USA
 Tel: 302 631 2638
 Fax: 302 631 2607
 Email: Michele.morgante@usa.dupont.com
 Sequences were trimmed to include only high quality bases; forward and reverse reads were assembled when significant overlaps were detected.
 Seq primer: M13univ and M13reverse
 Class: Shotgun.

FEATURES
 source 1. 847
 /organism="Zea mays"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="G-5c8"
 /sex="hermaphrodite"
 /tissue_type="leaf"
 /cell_type="young leaf"
 /dev_stage="seedling"
 /note="Vector: PCR-Script; Total genomic DNA was nebulized; ends were polished with Pfu polymerase and the fragments cloned into PCR-Script."

BASE COUNT 163 a 252 c 230 g 189 t 13 others

ORIGIN

Query Match 11.8%; Score 305.2; DB 17; Length 847;
 Best Local Similarity 77.1%; Pred. No. 2.3e-63;
 Matches 431; Conservative 0; Mismatches 114; Indels 14; Gaps 5;

39 CGGATCTCTCTCTTATTGCGAAGCCGACCGTGGCGCT-TTGGAGCGGTGGCGCAC 97
 25 CGGATCTCTCTCTTAAATGGGAAGCCGATCTGGAGACCGTGGCGCAC 84
 98 CGGACACTGTCGGTGGCACACCGGACAGTCAAGTCCCTTCCGACCGTGGCGTCCGCC 157
 85 CGGACA-TGTTGCGTGACACCGGACAGTCCGCTCCCTTCGACCGTGGCGTCCGCC 142
 158 AGTGTTCGCGCGGATCGCGGACAGCCGTTGGCCCGACCGGACCGTGGCGTCCGCC 217
 143 AGGTGTCGCGCGGACAGTCCGCGGACAGTCCGCTCCGCGGACCGTGGCGTCCGCC 202

Query Match	Similarity	11.5%	Score	297	DB	17	Length	710
Best Local	Similarity	75.4%	Pred.	No. 2.2e-61				
Matches	426	Conservative	0	Mismatches	125	Indels	14	Gaps
Qy	39	CGGATCTCCCTTCTTATTGTCGGAAGCCGACCGTTGG-CGCTTTGAGCCGTTGGGCGAC	97					
Db	123	CCGATTTCTCTTCTTAATAGGAAGCCGACCGTTGGTGAAGATTGGAGCCGTTGGCGAC	182					
Qy	98	CGGACACGTCCGGGTGCACACCGACAGTCAGGTGCCCCCTTCCGACCGTTGGCTCGGCC	157					
Db	183	CGGACA-TGTTTCGGGTGCACACCGACAGTCCGGTCCCCCTCTTCAAGCGTTGGCTCGGCC	241					
Qy	158	ACGTGT--TTGGCGGGATTCGGCGGGGACACCGTTGGGCCCGACCGACCGTTGGCTCACCG	215					
Db	242	ACGTGTCTCCCTTTTATTTATTCGGCGGGCGACCGTTGGGCCGACCGACCGTTGGCTCACCG	301					
Qy	216	GACAGTCCGGTGCACACCGACAGTCCGGTGAATATATAGCGGTACGCCGTTAATCACTTC	275					
Db	302	GACAGTCCGGTGCACACCGACAGTCCGGTGAATATATAGCGGTACGCCGTTAATCACTTC	361					
Qy	276	CCGAGACGACGAGTTCCCTTGAGCCAGCCCTTGGCGGACCGGACACTGTCCGGTGAACAC	335					
Db	362	CCGAGACGCGGACACTTCCGTCGAGGCGACCTTGGCGGACCGGACACTGTCCGGTGAACAC	421					
Qy	336	CGGACAGTCCGGTGAACCGACAGTCAAGAGCTGACTTTGGCTGAACAAAGTCACTTTAGTTC	395					

Qy	396	CAACTGATATTTTTCCTGTTTCAGACACTTAGACACAATATATAGTCTTAAACAATGT	455
Db	482	TTTCTCTCTCTTCTTGTTCTTAATACTTAGACAAGTATATTAGTACACAAAACCAATGT	541
Qy	456	ATTATTTCTGAGAAACATACCTTTATTACTTGTTTGAATCTTGTCAAC-----A	505
Db	542	ACTAAGACTTATAGACATACCTTTCCTTGTTCCTTTTGCGACTTGTGCATCATPACCATGA	601
Qy	506	TTTAAACACTTGGGCACTTGTTGTGAGACACTAAATACCAAAATATCTTAGAAATGGCCCA	565
Db	602	ATTCACTATTAGACACTTGTTGTGAGCGCTCAAAATCCCAAAATATCTTATTAATGGCCCA	661
Qy	566	GGGCACATTTCCCTTTTCAACAGCTCC	590
Db	662	GGGCACATCTCTCTCTTTCAATCTCC	686

RESULT 11
 BH837873/c 709 bp DNA linear GSS 28-MAY-2002
 LOCUS LMCN100005D09F Zea mays L. Zea mays genomic clone LMCN100005D09F,
 DEFINITION
 BH837873
 ACCESSION
 VERSION
 KEYWORDS
 GSS.
 SOURCE
 ORGANISM
 Zea mays.
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 (class; Panicoideae; Andropogoneae; Zea.
 1 (chr:nc1:550).

136 a 224 c 166 g 184 c

High quality sequence start: 60
High quality sequence stop: 555
Location/Qualifiers
1 700

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/organism="Zea mays"
/strain="873"
/db_xref="taxon:4577"
/clone="LMCR10005D09F"
/clone_1ib="Zea mays L."
/tissue_type="leaf"
/lab_host="RDH08"
/note="vector: pGEM-T easy; Site 1: Msc BC;
MethyI-filtration library; Nuclei DNA was completely
digested with Msc BC, size fractionated and transformed
to E.Coli DH10B."

```

BASE COUNT	165 a	188 c	203 g	152 f	1 others
ORIGIN					

Query Match	11.2%;	Score 289.2;	DB 17;	Length 709;
Best Local Similarity	74.5%;	Pred. No. 1.8e-59;		
Matches 408; Conservative	0;	Mismatches 128;	Indels 12;	Gaps 3

Qy	39	CGAATCTCTTCCTTAATTATTTGGGAGACCGGACCGTTGGCGCTTTGGAGACCGTTGGCCACG	98
Db	647	CGGATTTCTCTGGTTTAGATGTGAAGCTGACCAATATGGGATGGAGACCTTGGCCGA-C	589
Qy	99	GGAACATGTCCGGTGCACACCGGACAGTCAAGTCAAGTCCCTTCGACCCGTTGCTCGGCCA	158
Db	588	GGTGTAAAGGGGGGGTGCACACCGGAACAGGCGCGGTGCCCTTCGACCGTTGCTCGGCCA	529
Qy	159	CGTGTTTGCGCGGATTCGCGCGGCGAGACCCGTTGGCCCCGACCGACCGTTGGCTCACCGGAC	218
Db	528	CGTGTCCCGCGAGATTCGCGCGGCGGACCGTTGGCCCCGACCGTGGCTCACCGGAC	469
Qy	219	AGTCCGGTGCACACGACAGTCCGGTAATTATAGCCGTACGCCGTTAATCACTTCCG	278
Db	468	AGTCCGGTGCACACCGACAGTCCGGTAATTATAGCCGTACGCCGTTAATCACTTCCG	409
Qy	279	AGAGCAGCAAGTTCGCTCGAGCCAGCCGTCGGCGACCCGACACTGTCCGGTGAACACCCG	338
Db	408	AGAGGACCTCTTCGGCGGAGGCACTGTGGCACCCGACACTGTCCGGTGCACACCCG	349
Qy	339	ACAGTCCGGTGCACCCAGTCAAGCTGACTTTGGCTGAACAAATCATCTTTAGTCCAA	398
Db	348	ACAGTCCGGTGTCTCAGAACGAAAGCGCTGTGGCTGACACGCAACTTCTTTTC	289
Qy	399	CTTGATTTTTCGTTTCAGACTTGAACACAATACATTAATGTCTCTTAAACAATGATTT	458
Db	288	TCTTCTCTTCTCGTTTCTTAATCTTAAACAGATATATTAGTACCAAAACAATGTACT	229
Qy	459	AATTCTGAGAAATACCTTTAATCTTACTGTGTGTGACTTTGTCCACC-----ATT	508
Db	228	AATCTTAGAAACATACCTTTGTCTAGATTTGGACTTTGTCTATCCATGGGCAATGATTT	168
Qy	509	AACACTTGGGCACTTGTGTGTGAACACTAATATACAAATATCTTAGAATGGCCAAAGG	568
Db	168	CACATTTAAGCACTTGTGTT-GACACTCAATACCAAAATACTTAGAATGGCCAAAGG	110
Qy	569	CACATTTC 576	
Db	109	CACAGTTC 102	

RESULT 12	549 bp	DNA	linear	GSS	28-MAR-2002
LOCUS	BH774554				
DEFINITION	uzmb003f010f02k0	uzmb	unfiltered library	Ze	mays genomic clone
	uzmb003f010f02 5', DNA sequence.				
ACCESSION	BH774554				
VERSION	BH774554.1				
KEYWORDS	GSS.				
SOURCE	Ze				
ORGANISM	mays				

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 549)
Buddham, M. A., Freese, R. G., Bedell, J. A., Numborg, A. N., and Lakey, N. D.
GeneHreshers methylation filtered genomic sequences from maize
unpublished (2002)
Contact: Bedell JA
Contact: Numborg, N D

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

High quality sequence stop: 549.

```

1..549
/organism="Zea mays"
/cultivar="PMO17"
/db_xref="taxon:4577"
/clone="uzumb003f010f02"
/library="uzumb unfiltered library"
/notes="Organs: leaf; Vector: pBCSK(-); Site: 1; HincII; DNA
prepared from purified nuclei was randomly sheared,
fractionated by size, fractionated to enrich for the 0.5 to

```

BASE COUNT	120 a	142 c	127 g	160 t
ORIGIN				

Query Match	11.2%;	Score 288.4;	DB 17;	Length 549;
Best Local Similarity	81.9%;	Pred. No. 2.7e-59;		
Matches 367;	Conservative	1;	Mismatches 77;	Indels 3;
			Gaps	3

Qy	593	TGCCACACCGGACAGTCGCCGAGACCTCTGACCTCTGCTGTTCTAACTTCTGTGCGGGCACT	652
Db	80	TGCTGTACCGGACAGTCTGGAGACCTCTGACTTCTGCGCTTGACTTCTGACGCGGCACT	139
Qy	653	GTTTGGCACTATACGCTGTTTGGCAGTCGACCGGTGGCGCACAGAGAGCCATTGCTCCGTG	712
Db	140	GTTTATCATCTATTATCATCTGTGTCGAGATGACCATGGGCGGTAGAGGACGGTGTCCGCTG	199
Qy	713	GCTGACCGGACAGTCCCATGAAATTATAGCGGAGCGGGCCTGGAATPCCGAGTGGCC	772
Db	200	GCTCACCGGACAGTCCCGGTGAATTATAGCGGAGCGGGCCTCTGAATTCCGAGAGTGGCC	259
Qy	773	TGTTTGAAGGGGCGCTGGCGCTGCTGTCGACCGAACATGTATGCTGCGCCAAAATCAGCAC	832
Db	260	TGTTGGAAGGGGCGTCTGGCGCTAGTGCACCGGACACGTGTCGGTAGCGCCAAAATCAGCAC	319
Qy	833	ACTCAAGTCTTGGCTTCATTTTATATTTGTTGTGCTTAACTGATTTCTTT--TTGGTTGT	891
Db	320	ACTCA--TGCTGTGCTTCAAATTTGATTTGAGCCCTTCACTAAATTTCTTTCTTGTTGT	378
Qy	892	GTTGAACCTTATGACCTGAGATAATCAATCATCTAGACCAACTAGTTAGTCCATGTT	951
Db	379	GTTTAACTTATGACCTGAGATTAAGATCTAAGCAAACTAGTTAGTCCACATGTT	438
Qy	952	TGTGTTGATCGTCAACTATCTAAATCTATTTATAGAAAGTGGTTAACTTATCCCTT	1011
Db	439	TGTGTTGATCGTCAACCAACCAAAATCGA--TTATGAGAAATGGTTAACTTATCCCTT	497
Qy	1012	CAGCACACTCTATATAGTCTTGAGACC	1039
Db	498	CAATCTCTCCCTTTTGTGATTTAGTCC	525

RESULT 13			
BH836722			
LOCUS	BH836722	620 bp	DNA
DEFINITION	LMCR050003G04F Zea mays L. Zea mays genomic clone LMCRO50003G04F,		GSS 28-MAY-2002

ACCESSION DNA sequence.
 VERSION BH836722
 KEYWORDS BH836722.1 GI:21234600
 SOURCE GSS.
 ORGANISM Zea mays.
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 620)
 Kim,S.W., Yu,Y., Lee,M.C., Main,D. and Wing,R.A.
 Methy1-filtration genomic sequence from maize
 JOURNAL Unpublished (2002)
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total High Quality bases = 501
 Seq primer: TAAATACGACTCATTATAGCG
 Class: shotgun
 High quality sequence start: 7
 High quality sequence stop: 614.
 Location/Qualifiers
 1..620
 /organism="Zea mays"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="LMCR050003G04F"
 /clone_1lb="Zea mays L."
 /tissue_type="Leaf"
 /lab_host="DH10B"
 /note="Vector: pGEM-T easy; Site 1: Mcr BC;
 Methy1-filtration library; Nuclei DNA was completely
 digested with Mcr BC, size fractionated and transformed
 to E.Coli.DH10B."

FEATURES
 source
 BASE COUNT 133 a 137 c 156 g 133 t 1 others
 ORIGIN
 Query Match 11.0%; Score 284.2; DB 17; Length 620;
 Best Local Similarity 80.0%; Pred. No. 2.9e-58;
 Matches 380; Conservative 0; Mismatches 73; Indels 22; Gaps 3;
 QY 39 CGGATCTCTCTTCTTATTTGGCGAAGCCGCGTGGC-GCTTTGAGCGCGTGGCGCAC 97
 DB 121 CCGATTTCTTCTTCTTACCGCGAAGCCGCGTGGCAGCGAGCGCGTGGCGCAC 180
 QY 98 CGGACCTGTCGGGTGACACCGGACAGTGAAGTGGCCCTTCCGACCGTTGGCTGGCC 157
 DB 181 CGGACAT-----GTCGGGTGCCCCCTTTACCGCGTGGCTGGCC 220
 QY 158 ACCTGTTTCGCGCGATTCGCGCGAGACCGTGGCCGACCGGCGTGGCGTCAACCGGA 217
 DB 221 AGGTGTCGCGCGAGATCGCGCGCGCGACCGCTTGGCCGCGCGACCGTGGCTCAACCGGA 280
 QY 218 CAGTCCGCGTCAACACGACAGTCCGCGTGAATTATAGCCGTAGCCGTTAATCACTTCCC 277
 DB 281 CAGTCCGCGTCAACACGACAGTCCGCGTGAATTATAGCCGTAGCCGCGTGAATATCCC 340
 QY 278 GAGAGACGAGTTCGCGTGAAGCGCGTGGCGACCGGACACTGTCCGCTGAACACCG 337
 DB 341 GAGAGACGAGTTCGCGTGAAGCGCGTGGCGACCGGACACTGTCCGCTGAACACCG 400
 QY 338 GACAGTCCGCGTCAACAGTCAAGAGTGAAGTTCGCGTGAACAAAGTCATTTAGTTCCA 397
 DB 401 GACAGTCCGCGTCCCATATGAGAGAGTTCGCGTGAAGAGCA-AGACATTTCCA 459
 QY 398 ACTTGAATTTTCTGTTTCCAGACTTAAGACACATATCTTGTCTTAAACAATATAT 457
 DB 460 ATATGATCTTCTGTTTCCATCACTTAGACACATATATAGTCTTAAACAATATATAC 519

QY 458 TAACTGAGAAACATACCTTATCTTGTGATCTTGTCCACCATTTACA 512
 DB 520 TAACTGAGAAACATACCTTATCTTGTGATCTTGTCCACCATTTACA 574

RESULT 14
 BH839302 813 bp DNA linear GSS 28-MAY-2002
 LOCUS LMCR150010G08f Zea mays L. Zea mays genomic clone LMCR150010G08f,
 DEFINITION DNA sequence.
 VERSION BH839302
 KEYWORDS BH839302.1 GI:21237317
 SOURCE GSS.
 ORGANISM Zea mays.
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 813)
 Kim,S.W., Yu,Y., Lee,M.C., Main,D. and Wing,R.A.
 Methy1-filtration genomic sequence from maize
 JOURNAL Unpublished (2002)
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total High Quality bases = 494
 Seq primer: TAAATACGACTCATTATAGCG
 Class: shotgun
 High quality sequence stop: 667.
 Location/Qualifiers
 1..813
 /organism="Zea mays"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="LMCR150010G08f"
 /clone_1lb="Zea mays L."
 /tissue_type="Leaf"
 /lab_host="DH10B"
 /note="Vector: pGEM-T easy; Site 1: Mcr BC;
 Methy1-filtration library; Nuclei DNA was completely
 digested with Mcr BC, size fractionated and transformed
 to E.Coli.DH10B."

FEATURES
 source
 BASE COUNT 172 a 240 c 185 g 216 t
 ORIGIN
 Query Match 11.0%; Score 283.2; DB 17; Length 813;
 Best Local Similarity 78.8%; Pred. No. 5.1e-58;
 Matches 462; Conservative 0; Mismatches 88; Indels 36; Gaps 9;
 QY 37 TTCGATCTCTTCTTATTTGGCGAAGCCGCGTGGCGCTTGGAGCGCGTGGCGCA 96
 DB 87 TCGGATTTCTTCTTCTTATTTGGCGAAGCCGCGTGGAGATTCAAGAGCGTGGCGCA 146
 QY 97 CGGACCTGTCGGGTGACAC-----GACAGTGAAGTGGCCCC 137
 DB 147 CGGACCTGTCGGGTGACAC-----GACAGTGAAGTGGCCCC 206
 QY 138 TTCGACCTTGGCTCGGACAGTGTTCGCGGATCGCGCGACAGACCGTGGCGCGCA 197
 DB 207 TTTTAACTGTTGGCTTGCACAGTGTTCGCGGCGGAGTTAGCGCGCGATTTAGCGCGG 266
 QY 198 CCGACCTTGGCTTCAACGAGTCCGCTGCA-CACGACAGTCCGCGTGAATTATAGCC 256
 DB 267 CCGACCTTGGCTTCAACGAGTCCGCTGCA-CACGACAGTCCGCGTGAATTATAGTC 326
 QY 257 GTAGCGCGTGAATCACTTCCGAGAGAGAGTTCGCGTGAAGCGCGCGCGCGCACCGG 316
 DB 327 GTAGCGCGCGCA-GGAACCGAGAGAGCGCGTTCACAGAGCGCGCGCGCACCGG 385

QY 317 AACTGTCGGTGACACCGGACAGTCGGTGACCCCACTGAGAGTCACTTTGGCTGA 376
 DB 386 AACTGTCGGTGACACCGGACAGTCGGTGACCCCACTGAGAGTCACTTTGGCTGA 444
 QY 377 ACAAAGCATCTTTAGTTCCAACTGATTTTCTTTTCCAGACACTTAACACAATACA 436
 DB 445 GCTAGCCAAAGTCTTTTCCAAATGGCTTTCTTTCTTTAGAGCTTAACACAATACA 504
 QY 437 TTA-GTCTTAAACAAATGATTAATTTGAGAAACATACC-TTATATCTGTTGTATC 494
 DB 505 TTAGTCTCCACTACAAATGACTTAAGCTTAGAAACATACCTTTTACTCTTGAATTTGCAC 564
 QY 495 TTTGTCCACCAT-----TTAACACTTGGGCACTGTGTTGACACATAATACCA 544
 DB 565 TTTGTCCACTTGGGCACTGTGTTGACACATAATACCACTGTGTTG-CACTCATTTACCA 623
 QY 545 AATACTTGAATGGCCCAAGGACATTTCCCTTCAACAGTCC 590
 DB 624 AATACTTGA-ATATGCCAGAGGACATTTCTTTTCATCTTCC 668

RESULT 15

BH873660/c

618 bp DNA linear GSS 05-AUG-2002

hp46b1.b1 WGS-Zmaysf (JMI07 adapted methyl filtered) Zea mays

genomic clone hp46b1 5', DNA sequence.

BH873660

BH873660.1

GI:22109557

GSS.

Zea mays.

ORGANISM

Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 618)

Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,

Karzenbuser,F., King,L., Miller,B., Muller,S., Nascimento,L.,

Zuavev,T., McCombie,W.R. and Martienssen,R.A.

Genomic shotgun sequences from Zea mays (methyl-filtered)

Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: hp46 row: b column: 11

Seq primer: -21M13UnivFwd

Class: shotgun

High quality sequence stop: 618.

Location/Qualifiers

1. 618

/organism="Zea mays"

/cultivar="B73"

/db xref="taxon:4577"

/clone="hp46b1"

/clone_lib="WGS-Zmaysf (JMI07 adapted methyl filtered)"

/lab_host="JMI07 or DHSa"

/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;

The vector was digested with XbaI and one nucleotide was

added by fill in in the recessive 3' end. The genomic DNA

was nebulized, end repaired, adaptor ligated and size

fractionated using sephadex. The resulting fragments were

between 0.8 and 3 kb and were cloned into the vector

(.x/y reads in M13mp19, .b/g reads in pUC19). The same

ligation was transformed in either JMI07 or DHSa."

BASE COUNT

ORIGIN

165 a 113 c 168 g 172 t

Query Match

Best Local Similarity 10.9%; Score 282.2; DB 17; Length 618;

Matches 376; Conservative 0; Mismatches 48; Indels 15; Gaps 5;

QY 157 CACGTTTTCGGGCGGATCGCGCGGACAGCCGTTGGCCGACCGGCTCACCG 216
 DB 618 CATGTGCTCGCGGAGATCGCGGACAGCCGTTGGCCGCGGACCGGCTCACCG 559
 QY 217 ACAAAGCATCTTTAGTTCCAACTGATTTTCTTTTCCAGACACTTAACACAATACA 276
 DB 558 ACAAAGCATCTTTAGTTCCAACTGATTTTCTTTTCCAGACACTTAACACAATACA 499
 QY 277 CGAGGACGAGGATTCGCTGAGCCGAGCTGGCGGACCGGACACTGTCGGTGAACACC 336
 DB 498 CGAGGACGAGGATTCGCTGAGCCGAGCTGGCGGACCGGACACTGTCGGTGAACACC 439
 QY 337 GGAAGTCGCGTGACCCGAGTCAAGCT-GAATTGGCTGAACAAAGTCACTTATGTC 395
 DB 438 GGAAGTCGCGTGACCCGAGTCAAGCT-GAATTGGCTGAACAAAGTCACTTATGTC 381
 QY 396 CAATGATTTTCTGTTTCCAGACACTTAACACAATACATTAATCTTAAACAATGT 455
 DB 380 CAATGATTTTCTGTTTCCAGACACTTAACACAATACATTAATCTTAAACAATGT 321
 QY 456 ATTAATCTGAGAAACATACCTTTACTGTTGTACTTGTCCACCA----- 505
 DB 320 ACTAAGTCTG-GAAACATACCTTTTAACTGATTTGCACTTTGTCACCACTTGCATAG 262
 QY 506 TTTAACAATTGGGCACTTGTGTTGACACTTAATACCAAAATCTTAAGAAATGCCCCA 565
 DB 261 ATCAACAAAGGAACTTGTGTTG-CACTCAATACCAAAATCTTAAGAAATGCCCCA 203
 QY 566 GGGCACATTTCCCTTTCAA 584
 DB 202 GGGCACATTTCCCTTTCAA 184

Search completed: February 3, 2003, 16:08:28
 Job time : 2388 secs